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LOCUS      AR380482
DEFINITION      Sequence 1027 from patent US 6607879.
ACCESSION      AR380482
VERSION      AR380482.1 GI:40088116
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 1204)
AUTHORS      Cocks,B.G., Stewart,S.G. and Seilheimer,J.J.
TITLE      Compositions for the detection of blood cell and immunological response gene expression
PATENT      Patent: US 6607879-A 1027 19-AUG-2003;
FEATURES
source      1..1204
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/organism="Unknown"

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Best Local Similarity 100.0%; Pred. No. 3.2e-281;
Matches 1201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      481 GCTGACCGCTGGTCTCTCAGGCGCTGAGCCCAACCTGAGGCGCCCATTTACTTACTTA 540
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Db	601	GCAGCTGCTTGGCCGGGACTCTTCTTACCACTGGGACCCCAAGATCCCTGGCAGATC													
OY	661	CGATTTTATTTGGCAATCCCTTGTGATCTTCTGTGGAATGTTCTTGTGTTTACCCCTGGCCG													
Db	661	CGATTTTATTTGGCAATCCCTTGTGATCTTCTGTGGAATGTTCTTGTGTTTACCCCTGGCCG													
OY	721	GGCCCTGTTCCTCCATCAACGAGAAGGAATATAGATCAACAAGAGAAATCCTGTGGA													
Db	721	GGCCCTGTTCCTCCATCAACGAGAAGGAATATAGATCAACAAGAGAAATCCTGTGGA													
OY	781	GCTTGCAGAGCCCTTGTGCTTACAGCTGGCCCCAGAGGAGGAGGAGGCGCAGCATCCCAT													
Db	781	GCTTGCAGAGCCCTTGTGCTTACAGCTGGCCCCAGAGGAGGAGGAGGAGGCGCAGCATCCCAT													
OY	841	CCAGAGAGATTAACGAAAAACCGAGACCTTGGCTTCCCCCTGAGCCAGACACTTGGGTAG													
Db	841	CCAGAGAGATTAACGAAAAACCGAGACCTTGGCTTCCCCCTGAGCCAGACACTTGGGTAG													
OY	901	CTGCACCTACAGCCCTGGGCTCCACACCCGACCCGCGACATCCAGAGGAGAGTGAAC													
Db	901	CTGCACCTACAGCCCTGGGCTCCACACCCGACCCGCGACATCCAGAGGAGAGTGAAC													
OY	961	TGGCAGCCACAATGCACTGCACTGCCATCTCTTGTCAAGGGCCCTTCTCTGTATCAAGTACA													
Db	961	TGGCAGCCACAATGCACTGCACTGCCATCTCTTGTCAAGGGCCCTTCTCTGTATCAAGTACA													
OY	1021	GAGTGCCTTTTTCGAGACTGGGACGAGGACGAGACAAATATGATGAGTGTGAGAGTGGGA													
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Db	1081	GCAGGAGCCACGACGCTGGCGCTGGCGCTGACGAGGAGGCGGGGCTCGTGTGTTAAAA													
OY	1141	CACCTTCTGCTGCGAAGAACCCACATGCTACAGACGCGCAAAATTAAGTACAGATGAC													
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OY	1201	C 1201													
Db	1201	C 1201													
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DEFINITION	Sequence 1 from Patent WO03009862.														
ACCESSION	AX697951														
VERSION	AX697951.1	GI:29499010													
KEYWORDS															
SOURCE															
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.														
REFERENCE	Lucas, J., Dyalnas, D. and Briggs, K.														
AUTHORS	Agonists and antagonists of modumet for use in the treatment of														
TITLE	metabolic disorders														
JOURNAL	Patent: WO 03009862-A 1 06-FEB-2003;														
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Best Local Similarity	100.0%;	Prod. No. 3 2e-281;		
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RESULT 4
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DEFINITION AX818155
ACCESSION AX818155.1 GI:39723234
VERSION
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Ek,S., Borrebaeck,C.A. and Bhinger,M.
TITLE Treatment,diagnosis and imaging of disease
JOURNAL Patent: WO 03068268-A 26 21-AUG-2003;
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DEFINITION M63928.1 GI:180084
ACCESSION M63928.1
VERSION
KEYWORDS T-cell activation antigen CD27.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
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 AUTHORS Camerini, D., Walz, G., Loenen, W.A., Bors, J., and Seed, B.
 TITLE The T cell activation antigen CD27 is a member of the nerve growth
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 JOURNAL J. Immunol. 147 (9), 3165-3169 (1991)
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 PUBMED 1655907
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 Qy 1081 GCAGAGGCCCAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 Db 1081 GCAGAGGCCCAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 Qy 1141 CACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 Db 1141 CACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 Qy 1201 C 1201
 Db 1201 C 1201
 RESULT 6
 LOCUS BC012160 1323 bp mRNA linear PRI 29-JUN-2004
 DEFINITION Homo sapiens tumor necrosis factor receptor superfamily, member 7,
 mRNA (cDNA clone MGC:20393 IMAGE:4575359), complete cds.
 ACCESSION BC012160
 VERSION BC012160.1 GI:15082490
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1323)
 AUTHORS Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Cabavant, T.L.,
 Scheetz, T.E., Browne, M.J., Udell, T.B., Toshyaki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Whillany, S.J., Bosak, S.A., McSwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Holyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Db 1118 GAGTGCCTTTTGAGAGCTGGCAGAGGACGAGCAAAATATGATGAGGTGAGAGTGAGAA 1177
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 Db 1178 GCAGAGGCCCAAGCAGCTGGCTGGCTGTCAGAGAGGGCGGGGCTCTGTGTTTAAACA 1237
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 Db 1238 CACTTCCTGCTGGAGAAAGCCCAATGCTTACAGAGGGGCAAAATAATGAAGATGAC 1297
 Qy 1201 C 1201
 Db 1298 C 1298

RESULT 7
 LOCUS CQ721686 1204 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 7620 from Patent WO2068579.
 ACCESSION CQ721686
 VERSION CQ721686.1 GI:42282543
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Venter, C.J., Adams, M.C., Li, P.W., and Myers, B.W.
 Kites, such as nucleic acid arrays, comprising a majority of
 humenexons or transcripts, for detecting expression and other uses
 thereof
 Patent: WO 02068579-A 7620 06-SEP-2002;
 PE Corporation (NY) (US)
 Location/Qualifiers
 source 1..1204
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

JOURNAL
 Patent: WO 02068579-A 7620 06-SEP-2002;
 PE Corporation (NY) (US)
 Location/Qualifiers

ORIGIN
 Query Match 99.9%; Score 1199.4; DB 6; Length 1204;
 Best Local Similarity 99.9%; Pred. No. 7.9e-281;
 Matches 1200; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGCAAAAGAGAGCAGCAGCGCCAGCTTGAAGTGTCTAACTCCAGAGGCCAGCAT 60
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 Db 61 CAGCACTGGGCAAGAAAGAGAGCCGCTGGGAGGAGCCATGGCAACGGCCATCCCTG 120
 Qy 121 GTGGCTGTGCGTTCTGGGAGCCCTGGTGGGGCTCTCAGTACTCCAGGCCCAAGAGCTG 180
 Db 121 GTGGCTGTGCGTTCTGGGAGCCCTGGTGGGGCTCTCAGTACTCCAGGCCCAAGAGCTG 180
 Qy 181 CCCAGAGAGGCACTACTGAGGCTCAGGAAAGCTGTGCTGCAGATGTGTAGGCCAGAGAC 240
 Db 181 CCCAGAGAGGCACTACTGAGGCTCAGGAAAGCTGTGCTGCAGATGTGTAGGCCAGAGAC 240
 Qy 241 ATTCCCTGTGAAGAGACTGTGACCAAGATGAAGAGCTGTCAATGTGTATCTTTCATACC 300
 Db 241 ATTCCCTGTGAAGAGACTGTGACCAAGATGAAGAGCTGTCAATGTGTATCTTTCATACC 300
 Qy 301 GGGGGTCTCCTTCTCTCTGACCAACAACCCGGCCCACTGTGAGAGCTGTGGGCACTG 360
 Db 301 GGGGGTCTCCTTCTCTCTGACCAACAACCCGGCCCACTGTGAGAGCTGTGGGCACTG 360
 Qy 361 TAACTCTGTCTTCTGTGCTGCACTGCACTCATCACTGCCAATGTGATGTGCTGTG 420
 Db 361 TAACTCTGTCTTCTGTGCTGCACTGCACTCATCACTGCCAATGTGATGTGCTGTG 420
 Qy 421 CAATGCTGTGCAATGCAAGGAGCAAGAGATGCAACGAGTGTATCTTCTTCAAAACCTTC 480

Db 421 CAATGCTGTGCAATGCAAGGAGCAAGAGATGCAACGAGTGTATCTTCTTCAAAACCTTC 480
 Qy 481 GCTGACCGCTGGTGTCTCAGGCGCTGAGCCCAACCTTCAGGCCCACTTACCTTA 540
 Db 481 GCTGACCGCTGGTGTCTCAGGCGCTGAGCCCAACCTTCAGGCCCACTTACCTTA 540
 Qy 541 TGTCAATGAGATGTCTGAGAGGCCAGAGACAGTGGGCAATGCAAGCTGTGATCTTCA 600
 Db 541 TGTCAATGAGATGTCTGAGAGGCCAGAGACAGTGGGCAATGCAAGCTGTGATCTTCA 600
 Qy 601 GCAGTGGCGTGGCGGAGCTCTCTTCTACCACTGGGCCCAACCAAGATCCCTGTGAGCTC 660
 Db 601 GCAGTGGCGTGGCGGAGCTCTCTTCTACCACTGGGCCCAACCAAGATCCCTGTGAGCTC 660
 Qy 661 CGATTTTATTCGATCTCTGTGATCTTCTGGAATGTTCTTGTTTTCACTTGCCGG 720
 Db 661 CGATTTTATTCGATCTCTGTGATCTTCTGGAATGTTCTTGTTTTCACTTGCCGG 720
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 Qy 841 CCAGAGAGATTAACGAAACCGAGGCTGCTGCTCCCTGAGCAGCACTGGGGTAG 900
 Db 841 CCAGAGAGATTAACGAAACCGAGGCTGCTGCTCCCTGAGCAGCACTGGGGTAG 900
 Qy 901 CTGCACTAAGAGCCTTGGCTTCCACCCCAACCCGCGGACCTTCAAGAGAGATGAGACC 960
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 Db 961 TGGCAGCCCAACTGAGTCCCATCTCTTGTCAAGGAGCCCTTCTGTGTACAGTGTGAC 1020
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 Db 1021 GAGTGCCTTTTGAGAGCTGGCAGAGGACGAGCAAAATATGATGAGGTGAGAGTGAGAA 1080
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 Qy 1201 C 1201
 Db 1201 C 1201

RESULT 8
 LOCUS CQ869620 1300 bp DNA linear PAT 13-SEP-2004
 DEFINITION Sequence 41 from Patent WO2004074320.
 ACCESSION CQ869620
 VERSION CQ869620.1 GI:5199481
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Morris, D.W., Morris, D.W. and Malandro, M.S.
 Novel therapeutic targets in cancer
 Patent: WO 2004074320-A 41 02-SEP-2004;
 Sagres Discovery, Inc. (US)
 Location/Qualifiers

Query Match	99.9%	Score 1199.4	DB 6	Length 1300
Best Local Similarity	99.9%	Pred. No. 7.8e-281		
Matches 1200	Conservative	0	Mismatches 1	Indels 0
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Query Match	99.9%	Score 1199.4 <td>DB 6 <td>Length 1300</td> </td>	DB 6 <td>Length 1300</td>	Length 1300
Best Local Similarity	99.9%	Pred. No. 7.8e-281		
Matches 1200	Conservative	0	Mismatches 1	Indels 0
			Gaps	0
ORIGIN				
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	/organism="Homo sapiens"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:9606"			

QY	961	TGGACGCCAACAATGCAATGCCATCCTCTGTGACGGGCCCTTTCCTGTGACAGTGACA	1020
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QY	1021	GAGTGCCTTTTCGAGACTGCGAGGAGACGAGGACAATAATGATAGGTGAGAGTGGGAA	1080
Db	1118	GAGTGCCTTTTCGAGACTGCGAGGAGACGAGGACAATAATGATAGGTGAGAGTGGGAA	1177
QY	1081	GCAGAGCCCAACGACGCTGCGCCCTGCGCTGAGAGAGGGCGGGGCTCTGTGTGTAATAACA	1140
Db	1178	GCAGAGCCCAACGACGCTGCGCCCTGCGCTGAGAGAGGGCGGGGCTCTGTGTGTAATAACA	1237
QY	1141	CACCTTCCTGCTGCGAAAAAGACCACATGCTACAAGACGGGCAAAATTAAGTACAGATGAC	1200
Db	1238	CACCTTCCTGCTGCGAAAAAGACCACATGCTACAAGACGGGCAAAATTAAGTACAGATGAC	1297
QY	1201	C 1201	
Db	1298	C 1298	
RESULT 9			
LOCUS	AX778265	524 bp	DNA
DEFINITION	Sequence 422 from Patent WO03039443.	linear	PAT 14-JUL-2003
ACCESSION	AX778265		
VERSION	AX778265.1	GI:32695259	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1		
JOURNAL	Hafelrich, T.; Schoch, C., Kern, W., Kohlmann, A., Schmittger, S., Duga, M., Ellis, R., Brots, B. and Mergenthaler, S. Novel genetic markers for Leukemia Patent: WO 03039443-A 422 15-MAY-2003; Deutsches Krebsforschungszentrum (DE) ; Ludwig-Maximilian-Universitaet Muenchen (DE) ; Hafelrich, Torsten, PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)		
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	/mol_type="unassigned DNA"		
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Query Match	43.6%; Score 524; DB 6; Length 524;		
Best Local Similarity	100.0%; Pred. No. 1,7e-116;		
Matches 524; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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Db	1	CCTGTGACGCTCCGATTTTATTCGCAATCCTTGTGATCTTCTCTGSAATGTTCTGTTTT	60
QY	709	CACCTGACCGGGCCCTGTTCCTCCATCAACGAGAAATATGATCAACAAGGAGA	768
Db	61	CACCTGACCGGGCCCTGTTCCTCCATCAACGAGAAATATGATCAACAAGGAGA	120
QY	769	AAGTCTGTGAGAGCTTCAAGAGCCTTGTGTTACGCTGCCCCAGAGGAGAGAGGAG	828
Db	121	AAGTCTGTGAGAGCTTCAAGAGCCTTGTGTTACGCTGCCCCAGAGGAGAGAGGAG	180
QY	829	CACCATCCCATCCAGAGATTAACGAAAAACGGAGCCTGCTGCTCCCTGAGCCAG	888
Db	181	CACCATCCCATCCAGAGATTAACGAAAAACGGAGCCTGCTGCTCCCTGAGCCAG	240
QY	889	CACCTGCGTATGCTGACCTACAGCCCTGGGCTCACCCCAACCCCGCGACATCCAAAG	948
Db	241	CACCTGCGTATGCTGACCTACAGCCCTGGGCTCACCCCAACCCCGCGACATCCAAAG	300
QY	949	GAGAGTGAGACTGGACGACCAACTGCAATGCCATCCTTGTGACAGGCCCTTTCCTGT	1008


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Db      301 |GAGAGTGAAGCCTGGGAGCCACAACTGCACTCCCACTCTTGTGAGGGCCCTTTCTGT 360
Qy      1009 |GTAACAGTGAACAGATGCTCTTTTTCAGACTGTCAGAGGAGAGCAAAATATGATAGT 1068
Db      361 |GTACAGTGAACAGATGCTCTTTTTCAGACTGTCAGAGGAGAGCAAAATATGATAGT 420
Qy      1069 |GGAAGTGGAGAACAGAGCCAGAGCTGCGCTGCGCTGCGCTGCGAGAGGGCGGCTCT 1128
Db      421 |GGAGATGGAGAACAGAGCCAGAGCTGCGCTGCGCTGCGCTGCGAGAGGGCGGCTCT 480
Qy      1129 |GGTTGTAACACACTTCTGCTGTCGAAAGAACCCAGATGTACA 1172
Db      481 |GGTTGTAACACACTTCTGCTGTCGAAAGAACCCAGATGTACA 524

RESULT 10
MUSCD27A      1585 bp      mRNA      linear      ROD 25-SEP-1993
LOCUS      Mus musculus CD27 antigen (Cd27) mRNA.
ACCESSION      L24495.1 GI:403146
VERSION      CD27 antigen.
KEYWORDS      Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      1 (bases 1 to 1585)
JOURNAL      Gravesstein, L.A., Blom, B., Noltén, L.A., de Vries, E., van der
MEDLINE      Horst, G., Ossendorf, F., Boret, J. and Loenen, W.A.
PUBMED      Cloning and expression of murine CD27: comparison with 4-1BB,
COMMENT      another lymphocyte-specific member of the nerve growth factor
      receptor family
      Eur. J. Immunol. 23 (4), 943-950 (1993)

FEATURES
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      location/Qualifiers
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      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="B6/CBAF1J"
      /db_xref="taxon:10090"
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ORIGIN
Query Match      37.6%; Score 451.8; DB 10; Length 1585;
Best Local Similarity 73.2%; Pred. No. 5.2e-99;
Matches 633; Conservative 0; Mismatches 202; Indels 30; Gaps 3;

69 GGGGACAGAAAGAGCGCTGGGAGGAGACATGAGACGGCCACATCCCTGGTGTGT 128
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Qy      129 |GCGTTCTGGGAGCCCTGGTGGGCTCTCAGCTCTCAGGCCCCCAAGAGCTGCCAGAG 188
Db      206 |GCATCTGGGAGCCTTGATGAGACTCTCAGCTACCTACGCCCAAGAGCTGTCCAGACA 265
Qy      189 |GGCAGTACTGGGCTCAGAGAAAGCTGTGCTGCCAGATGTGTGAGCCAGAACTTCTCG 248
Db      266 |AACACTACTGAGACTGGGGAGAGACTGTGCGCGAGATGTGTGAGCCAGTATCAATTTCT 325
Qy      249 |TGAAGACTGTGACACGATAGAAAGCTGTCTCAGTGTATCTTGTGATACCGGGGCTCT 308
Db      326 |TGAAGACTGTGAGACAGAAAGCACTGTCTCAGTGTATCTTGTATACAGGAGCT 385
Qy      309 |CCTTCTCTCTGACACCAACCGGCGCCCACTGTGAGACTGTGCGCACTGTAACTCTG 368

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Db      386 |CCTTCTCTCAGACTACACACCCGCCCCCACTGCGAGAGCTGACGATGTAACTCTG 445
Qy      369 |GTCTTCTGTTGGCACTGACATCATCTGCTCCAAATGCTAGTGTCTTCCCAATGGCT 428
Db      446 |GTTTCTTATCCGCACTGACAGTCACTGACCAATGCTAGTGTGACAGCTTTCMAAAGCT 505
Qy      429 |GGCAGTGCAGGGGCAAGAGATGCAACGAGTGTGATCTCTTCCAAACCTTGCCTAGCG 488
Db      506 |GGCAGTGCAGGGAGCAAGATGTATGACAGATGTGACCTCTCTTAAACCTTGACCTACCA 565
Qy      489 |CTCGATCTGTCTAGGCTTGAAGCCACACCTTCAAGCCACCACTTATGTAGTGTG 548
Db      566 |GACAGCATCTGAGACCCGAGCCACAGCCACACCCACCTTACTTACCTATGACAGAG 625
Qy      549 |AGATGCTGAGAGCCAGAGACAGTGGGCAATGCACTGTGGCTGACTTCAAGCACTGC 608
Db      626 |AGAGAGC-----CATCTGCCCCCTTACA-----CAGGCACTTTC 658
Qy      609 |CTGCCCCGAGCTCTCTTACCCCACTGGGCAACCCCAAGATCCCTGTGAGCTCCGATTTTA 668
Db      659 |CAACTGCACTGTCTATAGCCAGCGGTATCCCATGAGCCCTGTGACAGCTGGACTGCA 718
Qy      669 |TTGCACTCTTGTGATCTTCTGTGAATGTCTTGTTCCTTTCACCTGAGCCGGGCTGT 728
Db      719 |TCCGATCTTTTGTGACTTCTTCAAGATGTCTTATCTTTCCTGCTGGGTGCAATCTTGT 778
Qy      729 |TCTTCATCAACGAGAAATATATGATCAACAAAGAGAAAGTCTGTGAGAGCTTGCAG 788
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Qy      789 |AGCTTGTGTTTACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 848
Db      836 |AGCTTGTCTTACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 895
Qy      849 |ATTACGAAACCGAGAGCTGTGCTGCTCCCTGAGCCAGACACTTGGTGTGACTGACTA 908
Db      896 |ACTACGAAACCGAGAGCTGTGCTTCTTACCTTGAACCGGCTGTGTGAGAGAGAGAG 955
Qy      909 |CAGCCTGAGCTTCCACCCCAAGCCG 933
Db      956 |ACGAGAGGCGCATCCACAGAGACTCT 980

RESULT 11
AC006064      172571 bp      DNA      linear      PRI 01-FEB-2003
LOCUS      Homo sapiens 12 PAC RP5-940U5 (Roswell Park Cancer Institute Human
ACCESSION      PAC library) complete sequence.
VERSION      AC006064.10 GI:28191361
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
      1 (bases 1 to 172571)
      Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
      Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Ayale, M., Banks, T.,
      Barbarta, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
      Bouck, J., Bowls, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P.,
      Buhay, C., Burch, P., Burkett, C., Butrell, K.L., Byrd, N.C.,
      Carron, T.P., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
      Chen, G., Chen, R., Chen, Z., Chin, D., Chowdhury, I., Christopoulos, C.,
      Cleveland, C.D., Cox, C., Coyle, M.D., Dathenbury, S.R., David, R.,
      Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
      Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
      Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
      Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S.,
      Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P.,
      Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N.,
      Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
      Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P.,
      Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hughes, M.,

```

Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulik, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, B., Kelly, S., Khan, U., King, L., Korvab, J., Kovar, C., Kratovic, J., Kureishi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichare, O., Lien, C., Liu, U., Liu, W., Louised, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maneshwar, M., Mapu, P., Maronde, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawney, B., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzner, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Ogih, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, D., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoochert, N., Sison, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tamsey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vaequez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kuchelapatti, R., Weinstock, G., and Gibbs, R.

TITLE

Direct Submission

REFERENCE

Unpublished

AUTHORS

Worley, K.C.

JOURNAL

Submitted (26-NOV-1998)

REFERENCE

Submitted (07-APR-1999)

AUTHORS

Worley, K.C.

JOURNAL

Submitted (15-MAR-2002)

REFERENCE

Submitted (01-FEB-2003)

AUTHORS

Worley, K.C.

JOURNAL

Submitted (01-FEB-2003)

REFERENCE

Submitted (01-FEB-2003)

AUTHORS

Worley, K.C.

JOURNAL

Submitted (01-FEB-2003)

REFERENCE

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JOURNAL

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JOURNAL

Submitted (01-FEB-2003)

REFERENCE

Submitted (01-FEB-2003)

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Worley, K.C.

JOURNAL

Submitted (01-FEB-2003)

REFERENCE

Submitted (01-FEB-2003)

AUTHORS

Worley, K.C.

JOURNAL

Submitted (01-FEB-2003)

REFERENCE

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AUTHORS

Worley, K.C.

JOURNAL

Submitted (01-FEB-2003)

REFERENCE

Submitted (01-FEB-2003)

AUTHORS

Worley, K.C.

JOURNAL

Submitted (01-FEB-2003)

REFERENCE

Submitted (01-FEB-2003)

AUTHORS

Worley, K.C.

FEATURES

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repeat_region

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu/8088/quality.info/genbank.annotation.html>.

FEATURES

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8411. 8539

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Best Local Similarity 99.8%; Pred. No. 1.5e-97;
Matches 445; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 8503 CCCCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8562
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DB 8563 CGACCATCCAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8622
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DB 8623 GGCCTTTCTGTGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8682
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DB 8683 ATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8742
QY 1116 GGGCGGGGGGCTGTGTGTAAACACACTTCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1175
DB 8743 GGGCGGGGGGCTGTGTGTAAACACACTTCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8802
QY 1176 CGGCAAAATTAAGTACAGATGACC 1201
DB 8803 CGGCAAAATTAAGTACAGATGACC 8828

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RESULT 12
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LOCUS AY504961 Homo sapiens tumor necrosis factor receptor superfamily, member 7
DEFINITION (TNFRSF7) gene, complete cds.
ACCESSION AY504961
VERSION AY504961.1 GI:40288428
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 10529)
AUTHORS Livingston,R.U., Rieder,M.U., Chung,M.-W., Ritchie,T.K.,
Olson,A.N., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D.,
Schackwitz,W.S., Sherwood,J.K., Sherwood,A.M., Leithauer,B.J. and
Nickerson,P.A.
Direct Submission
Submitted (16-DEC-2003) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: NIEHS-SNPe, Environmental Genome
Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
(URL: http://egp.gs.washington.edu).
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1051
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    ECACRNWCQCKECCDPLNPSTLAKSSQALSPHQPTHLPVSEMLKATIGHM
    QTLADPRLPARTLTHMPQRLCSSDPIRLVIFSGMLVFTLAGALFLQRRKXR
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    Best Local Similarity 99.6%; Pred. No. 5,8e-97;
    Matches 444; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

    QY 756 CAAACAAAGAGAAAGTCTGTGGAGCCCTGACAGACCTTGTCTTACAGCTGCCAGG 815
    DB 8151 CAGACAAAGAGAAAGTCTGTGGAGCCCTGACAGACCTTGTCTTACAGCTGCCAGG 8210
    QY 816 AGAGAGAGGACGACACCATCCCATCCAGAGGATTAACGAAGACGAGCCTGCTGCT 875
    DB 8211 AGAGAGAGGACGACACCATCCCATCCAGAGGATTAACGAAGACGAGCCTGCTGCT 8270
    QY 876 CCCCTGAGCCAGACCTGCGGTAGCTGACCTACAGACCTGACCTTCACACCCACCCCGC 935
    DB 8271 CCCCTGAGCCAGACCTGCGGTAGCTGACCTACAGACCTGACCTTCACACCCACCCCGC 8330
    QY 936 CGACCATCCAGAGGAGAGTGAACCTGCGAGCCCAACCTGCACTCCATCTCTTGTGAG 995
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    QY 996 GGCCCTTCTGTCGTACAGTGAACAGAGTGCCTTTTCGAGACTGGACGAGGACGAGACAA 1055
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Db      8511 GGGCGGGGGGCTCTGCTGTGTAACACACACTTCTGCTGCGGAAAGCCACATGCTACAGA 8570
QY      1176 GGGGCAAAATATAAGTGCAGATGACC 1201
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RESULT 13
LOCUS   CO869619 26815 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 40 from Patent WO2004074320.
ACCESSION CO869619
VERSION   CO869619.1 GI:51999480
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  Morris,D.W., Morris,D.W. and Malandro,M.S.
TITLE     Novel therapeutic targets in cancer
JOURNAL   Patent: WO 2004074320-A 40 02-SEP-2004;
           Sagres Discovery, Inc. (US)
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ORIGIN
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Best Local Similarity 99.6%; Pred. No. 5e-97;
Matches 444; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      756 CAAACAAAGAGAAAGTCTGTGAGAGCTTCGACAGCTTGTCTTACAGCTGCCCGAGG 815
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QY      816 AGAGAGAGGGACACACATCCCATCCAGAGAGATTACGAAACCGAGACCTGCTGCT 875
Db      16427 AGAGAGAGGGACACACATCCCATCCAGAGAGATTACGAAACCGAGACCTGCTGCT 16486
QY      876 CCCCTGAGGCACACCTGCGGTAGCTGACATACAGCCCTGCGCTCCACCCCAACCCCGC 935
Db      16487 CCCCTGAGGCACACCTGCGGTAGCTGACATACAGCCCTGCGCTCCACCCCAACCCCGC 16546
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QY      996 GGGCCCTTCTGTGTACCTGTGACAGTGCCTTTTTCGAGACTGGACGAGAGACAA 1055
Db      16607 GGGCCCTTCTGTGTACCTGTGACAGTGCCTTTTTCGAGACTGGACGAGAGACAA 16666
QY      1056 ATATGATGAGGTGGAGAGTGGAGAGAGCCAGCCAGCTGCGCTGCTGACAGA 1115
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QY      1116 GGGCGGGGGGCTCTGCTGTGTAACACACACTTCTGCTGCGGAAAGCCACATGCTACAGA 1175
Db      16727 GGGCGGGGGGCTCTGCTGTGTAACACACACTTCTGCTGCGGAAAGCCACATGCTACAGA 16786
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RESULT 14

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AC005840/c
LOCUS   AC005840 140026 bp DNA linear PRI 20-OCT-2000
DEFINITION Homo sapiens complete sequence of a PAC clone Rpl-102E24 containing
           SYB1, CD27, and SCNN1A genes.
ACCESSION AC005840
VERSION   AC005840.2 GI:10938025
KEYWORDS
SOURCE    HTG.
ORGANISM  Homo sapiens (human)
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  Montgomery,K.T., Lau,S.T. and Kucherlapati,R.
TITLE     High Throughput Sequencing of Human Chromosome 12
JOURNAL   Unpublished
           2 (bases 1 to 140026)
REFERENCE
AUTHORS  Montgomery,K.T., Lau,S.T. and Kucherlapati,R.
TITLE     Direct Submision
JOURNAL   Submitted (22-OCT-1998) Department of Molecular Biology, Albert
           Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY
           10461, USA
           3 (bases 1 to 140026)
           10461, USA
REFERENCE
AUTHORS  Montgomery,K.T., Lau,S.T. and Kucherlapati,R.
TITLE     Direct Submision
JOURNAL   Submitted (20-OCT-2000) Department of Molecular Genetics, Albert
           Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY
           10461, USA
           On Oct 20, 2000 this sequence version replaced gi:3779004.
           -----Genome Center:
           Albert Einstein College of Medicine
           Code: AECOM
           Web site: http://sequence.aecom.yu.edu/chr12/
           Contact: jhan@sequence.aecom.yu.edu

COMMENT
CLONE LENGTH: This sequence represents the entire insert of this
clone unless otherwise noted. If there are overlapping clones, the
overlaps are noted in the beginning and end of the Features
listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550).
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human sequences.
Genes and Regions of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST
and cDNA sequences in Unigene. Genes demonstrate at least two exons
flanked by consensus splice sites that maintain sequence continuity
across the splice junctions. Sequences that are not identical
matches are annotated as similar.

SEQUENCING READ COVERAGE: Attempts are made to complete double
stranded sequence for all regions. All sequence is completed to a
standard of coverage with a minimum of 3 reads with no ambiguities.
If the sequence coverage for a region does not meet this standard,
it is indicated in the annotation as Low Coverage. Low coverage
linkages are verified by PCR product size verification or
verification of forward and reverse reads from clones which span
the low coverage area.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated average error rate is less than 1 per 10,000
bases using the Consed quality parameter. Regions that do not
meet this requirement are annotated as Low Quality.

-----Summary Statistics
Center project name: Rpl-102E24
Sequencing vector: M13
Chemistry: Dye-terminator Big Dye; 100%
Assembly program: Phrap version 0.990119
Contig length: 140026
Fraction of Phrap value < 40: 0.0426
Error Rate in Consed: 0.56 per 10,000 bases
Number of N's in consensus: 1

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----- Distribution of Quality < 40 Bases:

#	0	5	10	15	20	25	30	35	40
1000								*	*
900								*	*
800								*	*
700								*	*
600								*	*
500								*	*
400						*	*	*	*
300					*	*	*	*	*
200				*	*	*	*	*	*
100		*	*	*	*	*	*	*	*
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----- Phrap Value Range

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Query Match 36.7%; Score 441.2; DB 9; Length 140026;

Best Local Similarity 99.3%; Pred. No. 9.3e-97; Mismatches 3; Indels 0; Gaps 0;

Matches 443; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 816 AGGAGAGGGCAGACATCCCATCCATCAGAGAGATTACGAAACCGGAGCCTGCTGCT 875
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 DB 33419 AGGAGAGGGCAGACATCCCATCCATCAGAGAGATTACGAAACCGGAGCCTGCTGCT 33360
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QY 876 CCCCCGAGCGACGACCTGCGGTAGCTGCACTACAGCCCTGGGCTCCACCCCAACCCGG 935
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 DB 33359 CCCCCGAGCGACGACCTGCGGTAGCTGCACTACAGCCCTGGGCTCCACCCCAACCCGG 33300
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QY 936 CGACCATCCAGGAGAGTAGAGACTGCGAGCGACCAACTGCAGTCCATCTCTTGTGAG 995

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